

Figure 1: Relative rates of transcription initiation for the 5' region of the rat H2A gene.

Panel A: Relative Rate (Sample A vs. Sample B)

Promoter	Sample A (Relative Rate)	Sample B (Relative Rate)
-375	~0.90	~0.90
-275	~1.00	~1.00
-257	~1.05	~1.00
-252	~1.05	~0.55
-237	~1.00	~1.10
-210	~0.95	~0.95
-193	~1.05	~0.95
-177	~0.90	~0.90
-154	~0.25	~0.30
-125	~0.15	~0.15
-114	~0.05	~0.05
-107	~0.05	~0.05
-98	~0.05	~0.05
Mock	0	0

Panel B: Relative Rate (with error bars)

Promoter	Relative Rate (approx.)
-375	1.00
-275	~0.65
-257	~0.82
-252	~0.80
-237	~0.70
-210	~0.75
-193	~0.58
-177	~0.55
-154	~0.48
-125	~0.45
-114	~0.32
-107	~0.60
-98	~0.42
-76	~0.12
-46	~0.08
-30	~0.02
-29	~0.02
-17	~0.02
-7	~0.02
Mock	0

Schematic Diagram: The diagram shows the 5' region of the rat H2A gene. The 5' cap is at the top. The 5' UTR contains the REPEAT II A and REPEAT II B regions. The REPEAT I B region is located downstream. The GATA and IE-2B motifs are located further downstream. The TATA box is located at the -30 position. The coding region starts at the -25 position. The Mock control is at the -7 position.

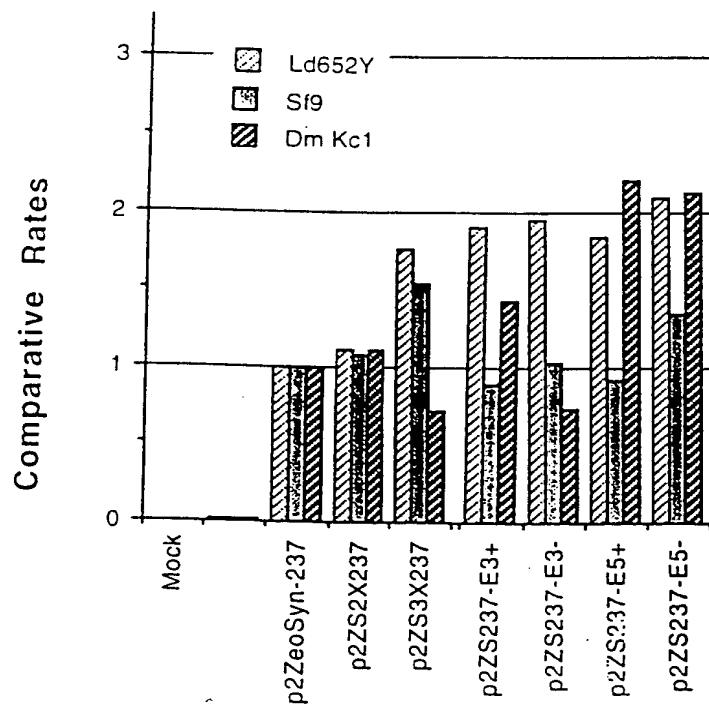
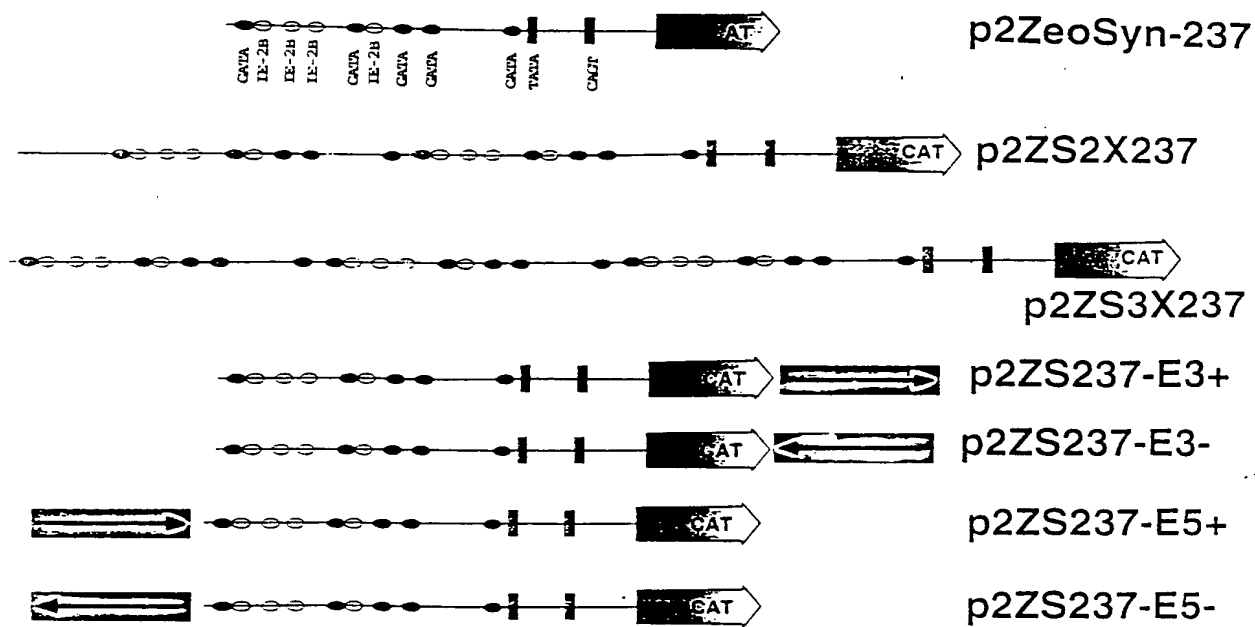


Figure 1b

-375D
 IIE-2CCCCA CCACCAACTT TTTTGCACTG CAAAAAACA CGCTTTTGCA CGCGGCCCCA TACATAGTAC AAACCTCAGC TTTTCGTAGAC TATTTTACAT
 IIE-N GATAAATTTA AAATGAATTT TTTTGCAATG CAAAAAGTT CACTTTTGCC TGACACTCCA TATACAGTAC AATCTCTACA AATCGTAG.C TATTTTATTA
 (REPEAT I A) (REPEAT II A)
 -275D -257D-252D -237D
 IIE-2 AAATAGTCTA CACGTTGTA TACGCTCCAA ATACACTACC ACACATTGAA CCTTTTGGCA GTGCAAAAAA GTACGTGTGC GCAGTCACGT AGCGCGGCTT
 IIE-N GAATAGTCTA CACTGTACGA TACGCTCCCA ATATACTACT ACACATCAAA CTTTTTGGCA TTACAAAAAA GTTCATTTTT G.....
 (REPEAT II B) (REPEAT I B)
 -177D -154D (E)
 IIE-2 426 (A) (B) -210D -193D (C) -177D (D) (E) 525
 TATCGGGTGC CGTCTGTCTCA CGTACCAATC ACATTATTCGG ACCGGACGAG TCTTGTCTTA TCGTGACAGG AGCCAGCTT CCGTGTGTGC TAACCGCAGC
 IIE-NCCTGGCA AGTTC.....CCCCACCAC TATGTCT.....
 (H) (GATA) (I) (GATA)
 -125D -114D(F)-107D -98D (G) -46D (I)
 IIE-2 (IE2B) (GATA) (IE2B) (GATA) (GATA) (GATA)
 CGGACGCAC TCCTTATTCGG AACAGACCG GCCTCCATAT CAGCGCGCGG TTATCTCATG CGCGTGACCG GACACGAGGC GCCCGTCCCG CTTATTCGCGC
 IIE-NTAT CAGTGTGTCA GTA.....
 +7D
 -30D, -29D -17D
 IIE-2 CTATAAATAC AGCCCGCAAC GATCTGCTAA ACACAGTTGA ACAGCATCTG TTACAGCGAC ACAACAT 692
 IIE-N GTATAAATAC AGCTGCGGTT CTACTCGTAA GCACAGTTCA ..AGCCTCAC AGCCTAGTGA ACAGTAT
 (TATA) (CAGT) ---5. IE-N
 ---5. IE-N

Figure 2a

[illegible]

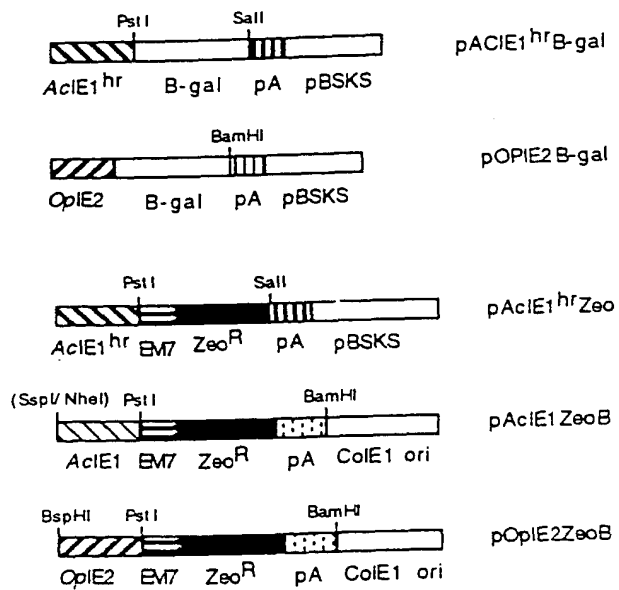


Figure 3

Kc1

Legend: 0 (open circle), 10 (filled circle), 25 (open square), 50 (open diamond), 75 (filled triangle), 100 (filled inverted triangle)

SL2

Legend: 0 (open square), 10 (filled square), 25 (open circle), 50 (filled circle), 75 (open triangle), 100 (filled triangle)

Sf9

Legend: 0 (open circle), 10 (filled circle), 25 (open square), 50 (filled square), 75 (open triangle), 100 (filled triangle)

Y-axis: Viable Cell Number ($\times 10^6/\text{ml}$)

X-axis: Time (days)

Figure 4a

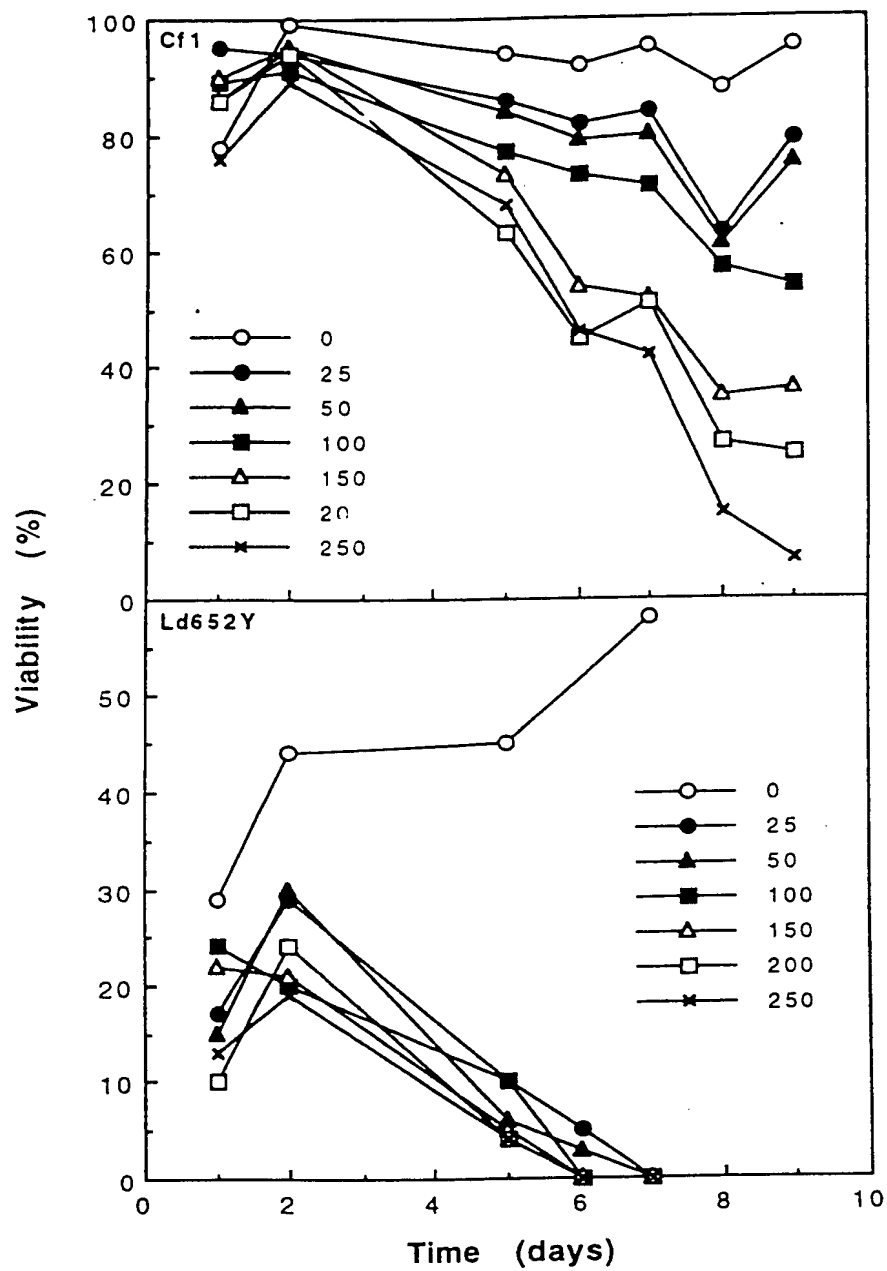


Figure 4b

Figure 1 consists of five vertically stacked line graphs, each representing a different *K. pneumoniae* strain. The y-axis for all graphs is 'Viable Cell Number (10⁶/ml)' and the x-axis is 'Time (Days)' from 0 to 8. Each graph shows the growth of the strain over time under various concentrations of an antibiotic (0, 50, 100, 250, 500, 1000, and 2000 units/ml). The legend for all graphs is as follows:

- 0: Open square
- 50: Filled square
- 100: Open circle
- 250: Filled circle
- 500: Open triangle
- 1000: Filled triangle
- 2000: Filled diamond

The strains and their corresponding antibiotic concentrations are:

- Kc1::pAclE1^{hr}Zeo**: 0, 50, 100, 250, 500, 1000
- Kc1::pAclE1ZeoB**: 0, 50, 100, 250, 500, 1000
- SL2::pAclE1^{hr}Zeo**: 0, 50, 100, 250, 500, 1000
- Sf9::pOplE2ZeoB**: 0, 250, 500, 1000, 1500, 2000
- Kc1::pOplE2ZeoB**: 0, 50, 100, 250, 500, 1000

In general, the growth of the strains is higher at lower antibiotic concentrations and decreases as the concentration increases. The growth is also generally higher in the first 4 days and then plateaus or slightly decreases.

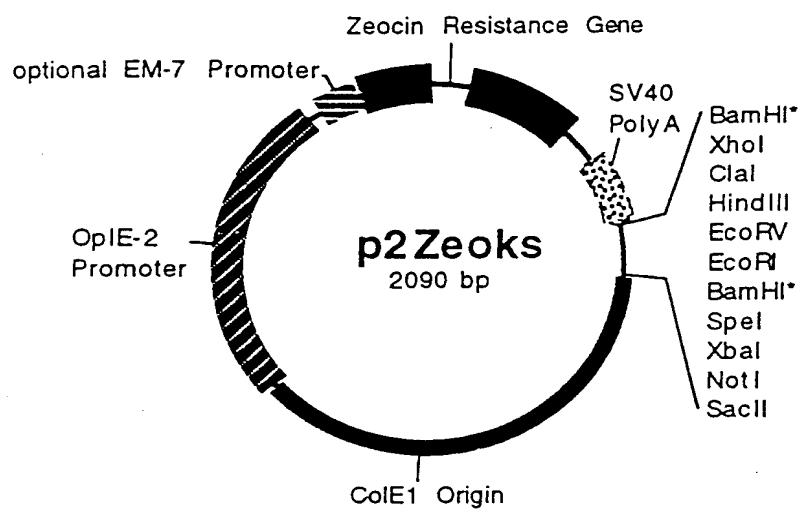


Figure 7

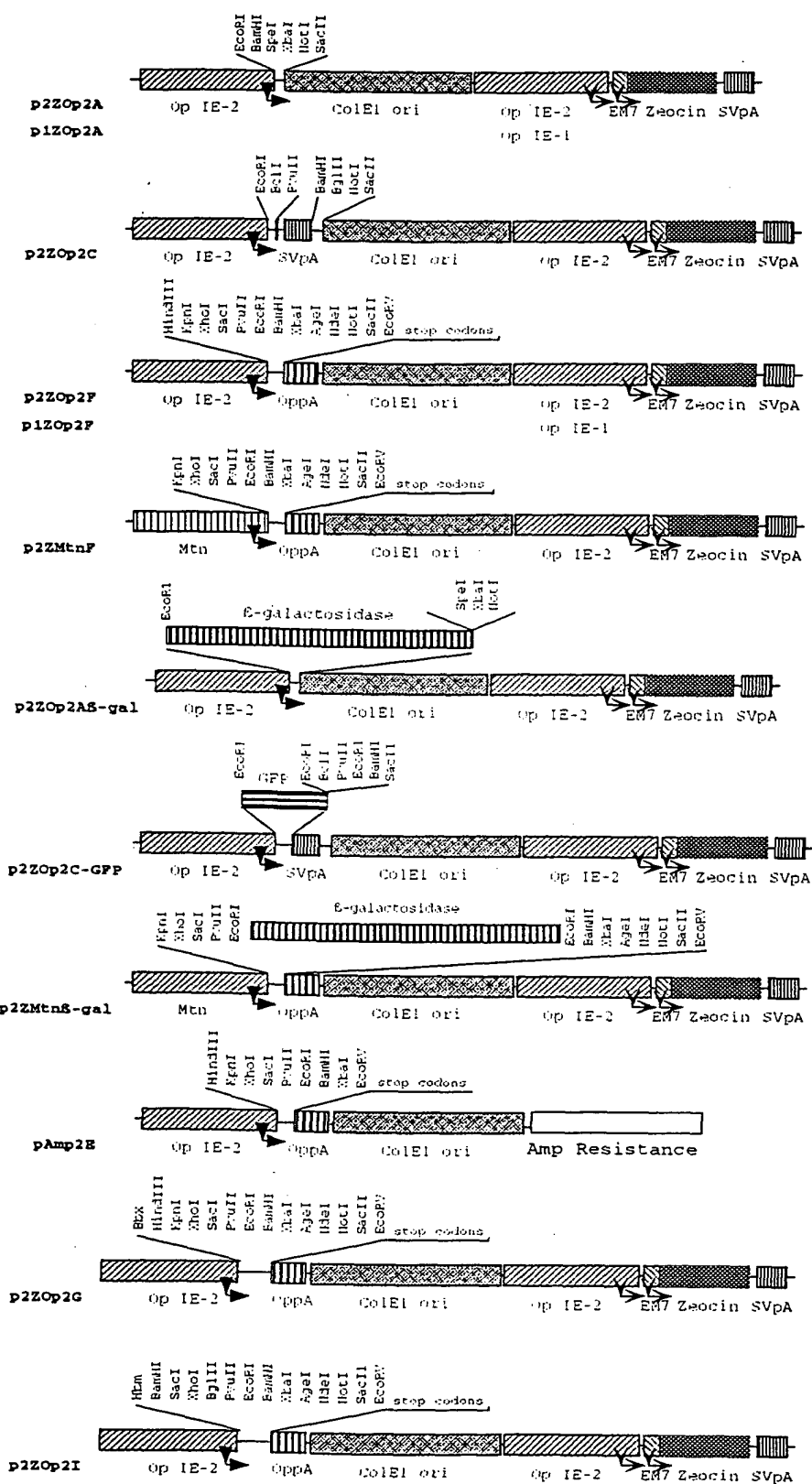


Figure 8a

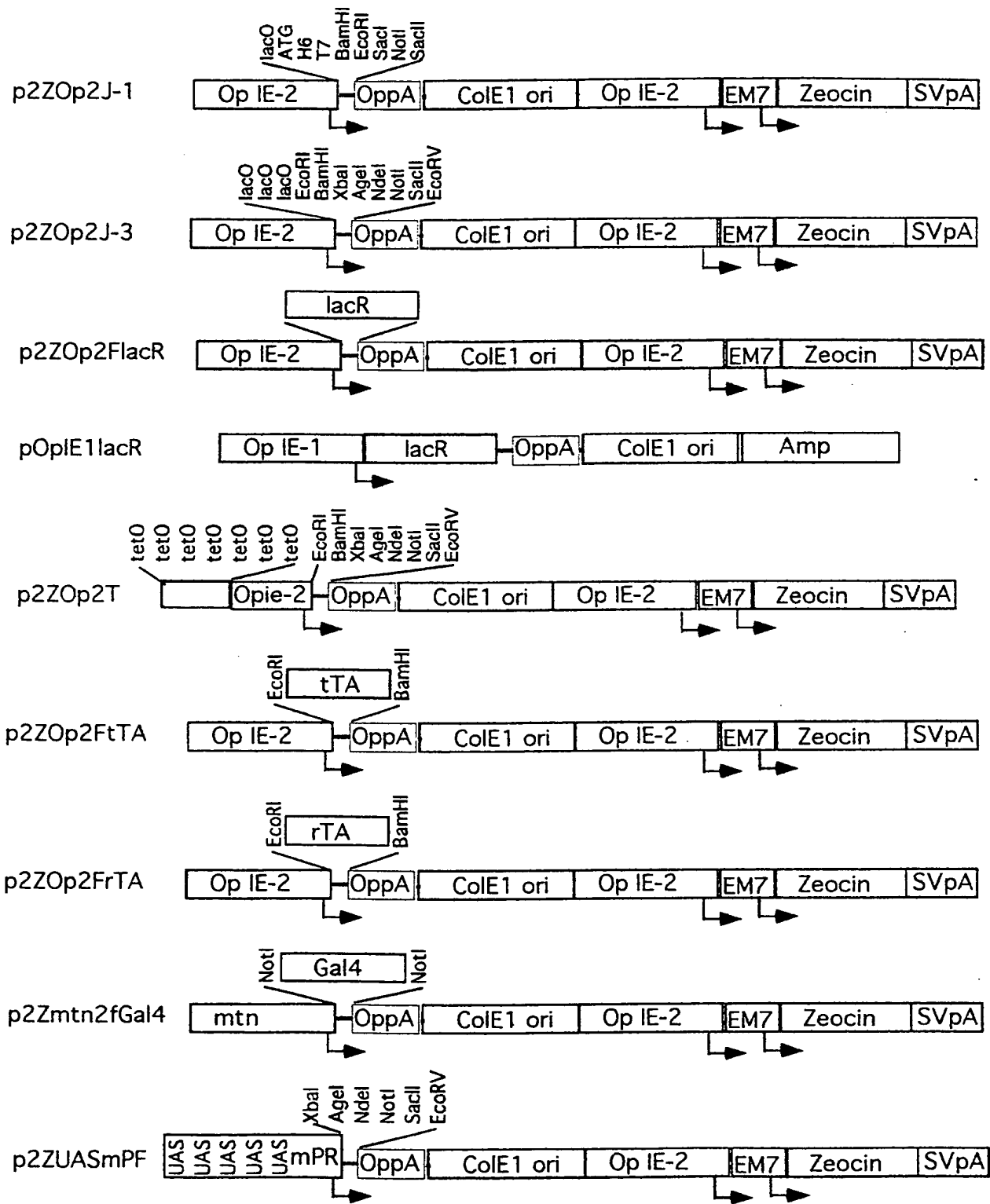


Figure 8b

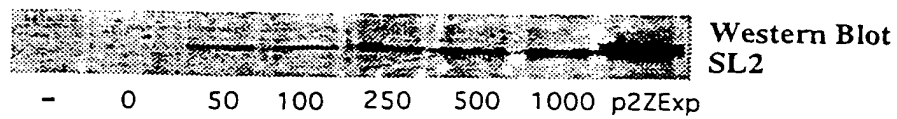
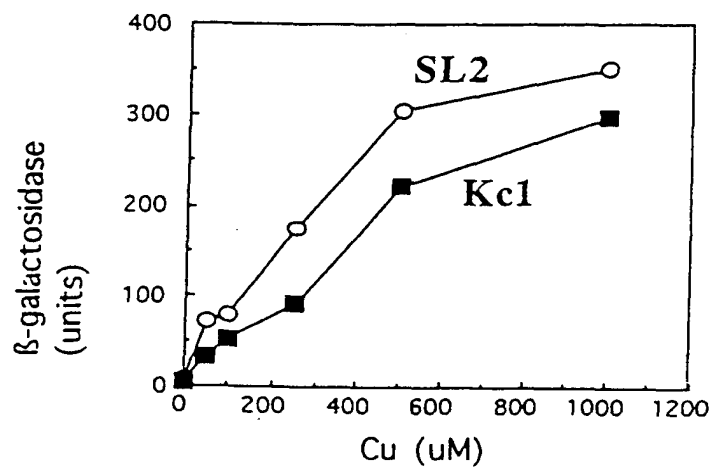


Figure 9

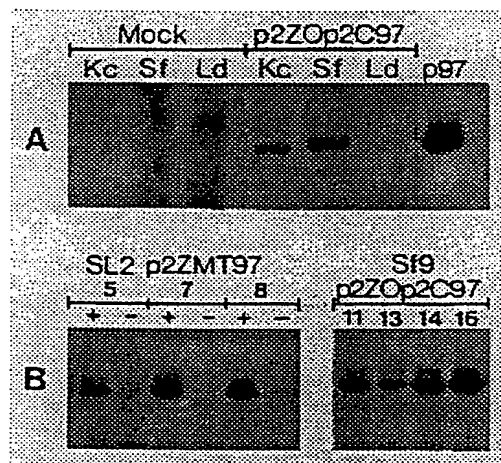



Figure 1 1



p87
GAC TAC GTG GCG CGC CTG GAA GGG ATG TCG TCT CAG CAG TTC TGC GCC ACA GCG GAT CCC GCG ACC CTC CTC CCG CTG CTC GTC GCG ACC CTC TGA
D Y V A A L E G M S S Q Q C S G A A P A P G A P L L P L A R L L P P A L *

120.7
GAC TAC GTG GCG CGC CTG GAA GGG ATG TCG TCT CAG CAG TTC TGC GCC ACA GCG ACC CTC GCG ACC CTC ATT TGA
D Y V A A L E G M S S Q Q C S G A A P A P G A P L I *

150.2
GAC TAC GTG GCG CGC CTG GAA GGG ATG TCG TCT CAG CAG TTC TGC GCC ACA GCG ACC CTC GCG ACC CTA TCT GAC TGA
D Y V A A L E G M S S Q Q C S G A A P A P G A P L S D *

60/90.3
GAC TAC GTG GCG CGC CTG GAA GGG ATG TCG TCT CAG CAG TTC TGC GCC ACA GCG ACC CTC GCG ACC ATT TGA
D Y V A A L E G M S S Q Q C S G A A P A P A P I *

120.6
GAC TAC GTG GCG CGC CTG GAA GGG ATG TCG TCT CAG CAG TTC TGC GCC ACA GCG ACC CCA TCT GAC TGA
D Y V A A L E G M S S Q Q C S G A A P S D *

150.5
GAC TAC GTG GCG CGC ATT TGA
D Y V A A I *

120.3
GAC TAC GTG GGT CTG ACT AAA TCT TAG
D Y V D L T F S *

chk typ 1 ----- C S G A G H K L I Q Q H L L V I T F V P F I I L G Q L Q G *
chk typ 2 ----- C S G A V S P E L C F O K P *

Figure 12b

MW
120.7
150.2
60/90.3
120.6
120.3
120.7
150.2
60/90.3
120.6
120.3
p97

169

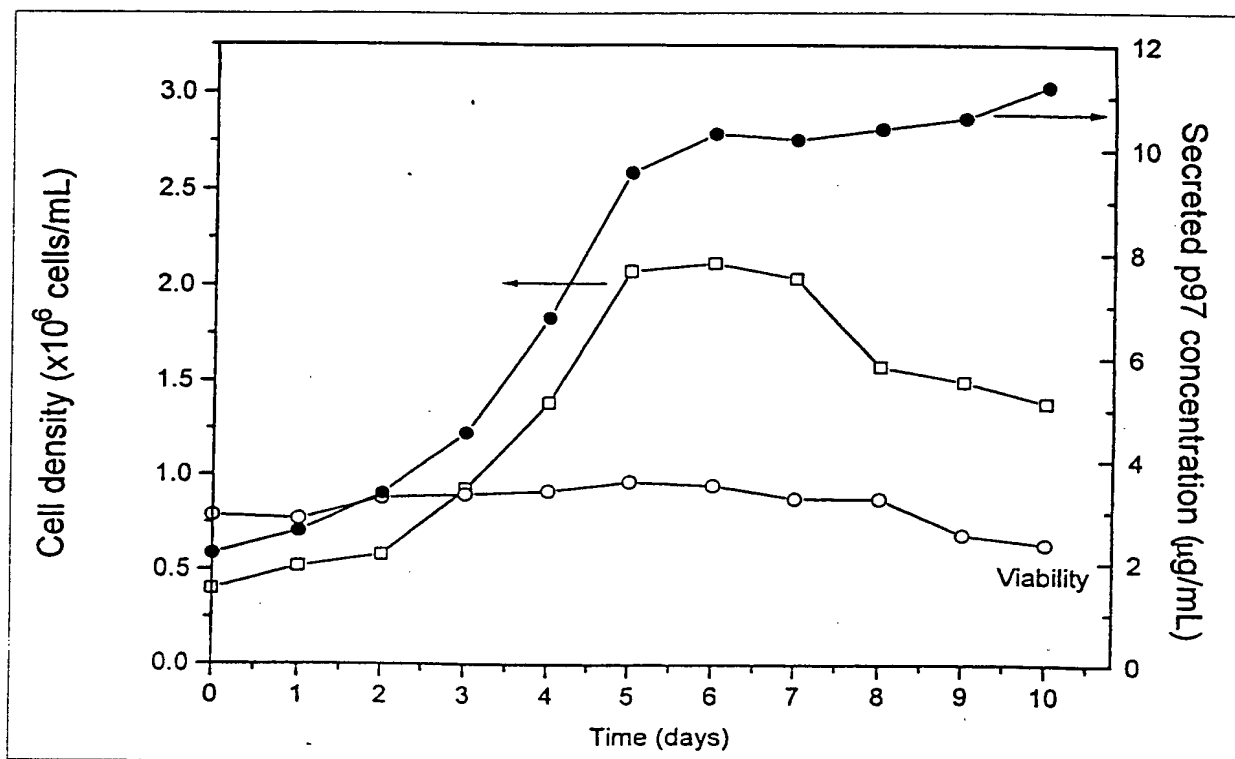


Figure 12d

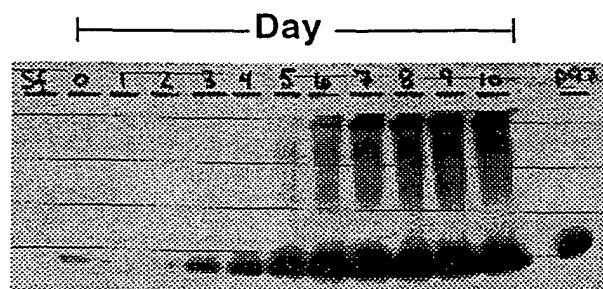


Figure 12e

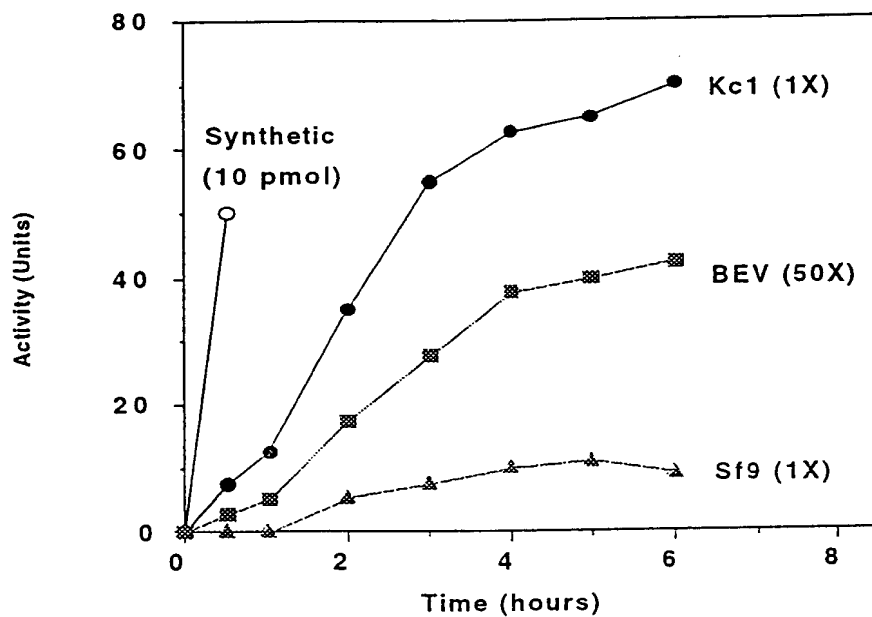


Figure 13a

Western blot analysis of the 12S protein in various yeast strains. The blot shows bands for Kc1 Control, Kc1 Transient, Kc1 Stable, SL2 Control, SL2 Transient, SL2 Stable, Hi5 Control, Hi5 Transient, Hi5 Stable, Ld Control, Ld Transient, Ld Stable, Sf9 Control, Sf9 Transient, and Sf9 Stable. Molecular weight markers are indicated on the left at 83, 62, and 47 kDa.

Figure 13b

Figure 14

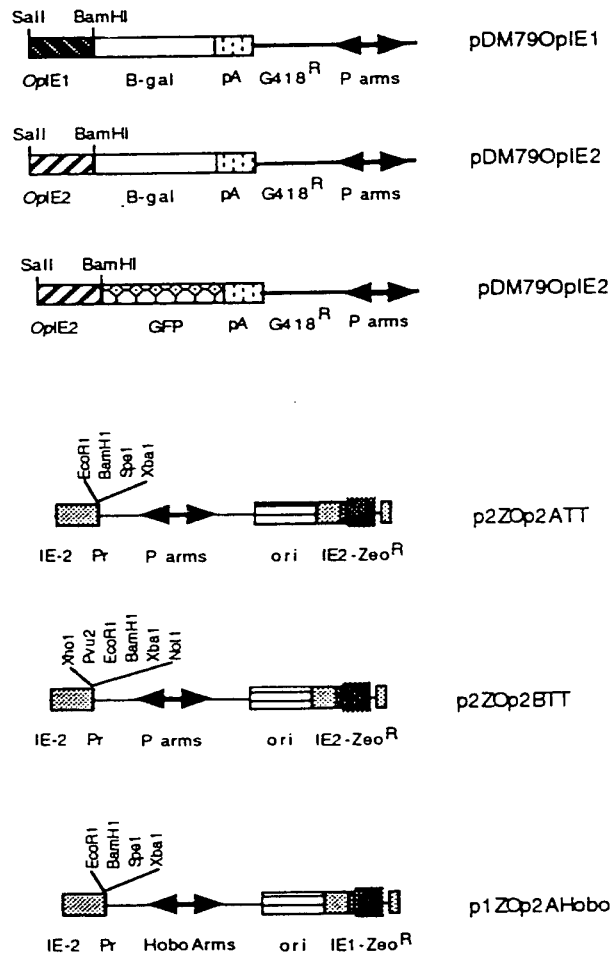


Figure 14

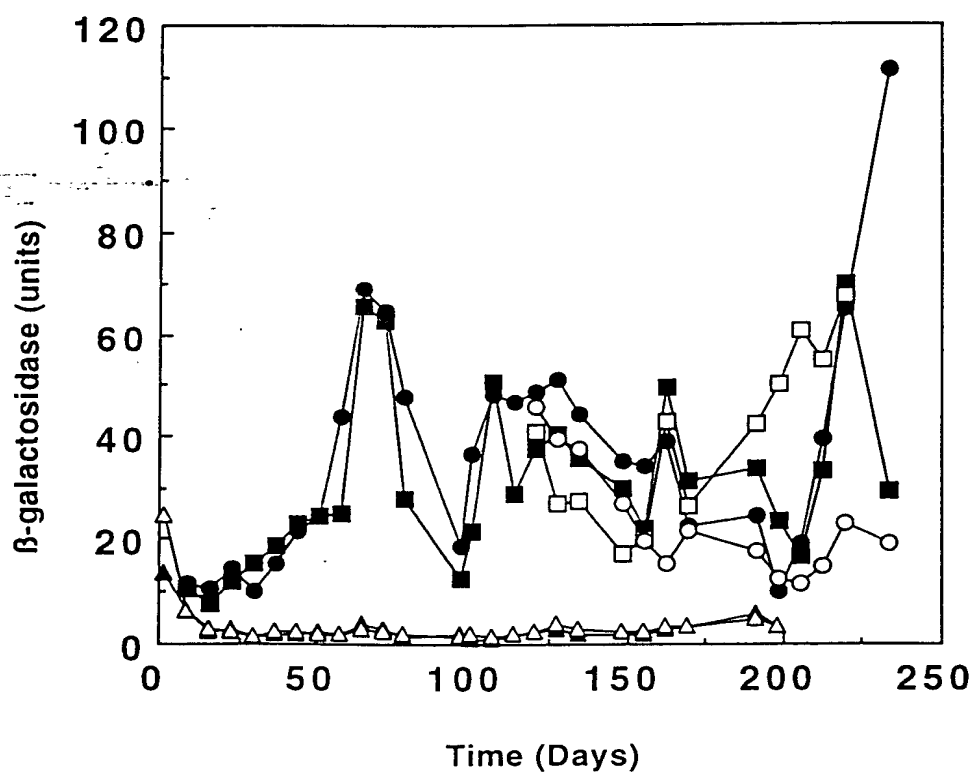


Figure 16a

5' P-element rescue

pDM79

CGACGGGACCACCTTATGTTATTTTCATCATGGGCCAGACCCACGTAGTCCAGCGGC...

79-2 Xho.6

CGACGGGACCACCTTATGTTATTTTCATCATGTCTCGAACCAACGAGAGCAGTATGC...

79-2 Xho.4

CGACGGGACCACCTTATGTTATTTTCATCATGGTACAGACATCTACTTCCCCCGCT...

79-1 Sph.1

CGACGGGACCACCTTATGTTATTTTCATCATGATCTTGCGCTTTAAAATGTGGAGTC...

3' P-element rescue

pDM79

CGACGGGACCACCTTATGTTATTTTCATCATGGCTCGGCCATTCTCATCGTGAGCTT...

79-2 kan.3

CGACGGGACCACCTTATGTTATTTTCATCATGAGCCAAACAGAAAGCAGAAAAGCTC...

79-2 kan.2

CGACGGGACCACCTTATGTTATTTTCATCATGGCCTGACCTAAGCAGATTTGACTGC...

79-2 kan.1

CGACGGGACCACCTT

CAACGCTACCTAATCTTAAGAACCA...

consensus

GNCYRRAC

Figure 16b

A dark, grainy, black and white photograph showing a close-up of a textured surface, possibly a wall or ceiling. A bright, circular light source is visible in the upper left corner, creating a strong contrast with the dark background. The overall image has a high-contrast, low-resolution appearance.

